



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/789,818

DATE: 08/06/2004

TIME: 14:14:07

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3 <110> APPLICANT: IBRAHIM, PRABHA
 4 KRUPKA, HEIKE
 5 KUMAR, ABHINAV
 6 MILBURN, MICHAEL V.
 7 SUZUKI, YOSHIHISA
 9 <120> TITLE OF INVENTION: PYK2 CRYSTAL STRUCTURE AND USES
 11 <130> FILE REFERENCE: 039363/1202
 13 <140> CURRENT APPLICATION NUMBER: 10/789,818
 14 <141> CURRENT FILING DATE: 2004-02-27
 16 <150> PRIOR APPLICATION NUMBER: 60/451,101
 17 <151> PRIOR FILING DATE: 2003-02-28
 19 <160> NUMBER OF SEQ ID NOS: 25
 21 <170> SOFTWARE: PatentIn Ver. 3.2
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 272
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Homo sapiens
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 32 Phe Gly Glu Val Tyr Glu Gly Val Tyr Thr Asn His Lys Gly Glu Lys
 33 20 25 30
 35 Ile Asn Val Ala Val Lys Thr Cys Lys Lys Asp Cys Thr Leu Asp Asn
 36 35 40 45
 38 Lys Glu Lys Phe Met Ser Glu Ala Val Ile Met Lys Asn Leu Asp His
 39 50 55 60
 41 Pro His Ile Val Lys Leu Ile Gly Ile Ile Glu Glu Pro Thr Trp
 42 65 70 75 80
 44 Ile Ile Met Glu Leu Tyr Pro Tyr Gly Glu Leu Gly His Tyr Leu Glu
 45 85 90 95
 47 Arg Asn Lys Asn Ser Leu Lys Val Leu Thr Leu Val Leu Tyr Ser Leu
 48 100 105 110
 50 Gln Ile Cys Lys Ala Met Ala Tyr Leu Glu Ser Ile Asn Cys Val His
 51 115 120 125
 53 Arg Asp Ile Ala Val Arg Asn Ile Leu Val Ala Ser Pro Glu Cys Val
 54 130 135 140
 56 Lys Leu Gly Asp Phe Gly Leu Ser Arg Tyr Ile Glu Asp Glu Asp Tyr
 57 145 150 155 160
 59 Tyr Lys Ala Ser Val Thr Arg Leu Pro Ile Lys Trp Met Ser Pro Glu
 60 165 170 175
 62 Ser Ile Asn Phe Arg Arg Phe Thr Thr Ala Ser Asp Val Trp Met Phe
 63 180 185 190
 65 Ala Val Cys Met Trp Glu Ile Leu Ser Phe Gly Lys Gln Pro Phe Phe



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66 195 200 205
 68 Trp Leu Glu Asn Lys Asp Val Ile Gly Val Leu Glu Lys Gly Asp Arg
 69 210 215 220
 71 Leu Pro Lys Pro Asp Leu Cys Pro Pro Val Leu Tyr Thr Leu Met Thr
 72 225 230 235 240
 74 Arg Cys Trp Asp Tyr Asp Pro Ser Asp Arg Pro Arg Phe Thr Glu Leu
 75 245 250 255
 77 Val Cys Ser Leu Ser Asp Val Tyr Gln Met Glu Lys Asp Ile Ala Met
 78 260 265 270
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 83 <211> LENGTH: 293
 84 <212> TYPE: PRT
 85 <213> ORGANISM: Artificial Sequence
 87 <220> FEATURE:
 88 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 89 pET15S protein containing PYK2
 91 <400> SEQUENCE: 2
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 93 1 5 10 15
 95 Arg Gly Ser His Met Ile Ala Arg Glu Asp Val Val Leu Asn Arg Ile
 96 20 25 30
 98 Leu Gly Glu Gly Phe Phe Gly Glu Val Tyr Glu Gly Val Tyr Thr Asn
 99 35 40 45
 101 His Lys Gly Glu Lys Ile Asn Val Ala Val Lys Thr Cys Lys Lys Asp
 102 50 55 60
 104 Cys Thr Leu Asp Asn Lys Glu Lys Phe Met Ser Glu Ala Val Ile Met
 105 65 70 75 80
 107 Lys Asn Leu Asp His Pro His Ile Val Lys Leu Ile Gly Ile Ile Glu
 108 85 90 95
 110 Glu Glu Pro Thr Trp Ile Ile Met Glu Leu Tyr Pro Tyr Gly Glu Leu
 111 100 105 110
 113 Gly His Tyr Leu Glu Arg Asn Lys Asn Ser Leu Lys Val Leu Thr Leu
 114 115 120 125
 116 Val Leu Tyr Ser Leu Gln Ile Cys Lys Ala Met Ala Tyr Leu Glu Ser
 117 130 135 140
 119 Ile Asn Cys Val His Arg Asp Ile Ala Val Arg Asn Ile Leu Val Ala
 120 145 150 155 160
 122 Ser Pro Glu Cys Val Lys Leu Gly Asp Phe Gly Leu Ser Arg Tyr Ile
 123 165 170 175
 125 Glu Asp Glu Asp Tyr Tyr Lys Ala Ser Val Thr Arg Leu Pro Ile Lys
 126 180 185 190
 128 Trp Met Ser Pro Glu Ser Ile Asn Phe Arg Arg Phe Thr Thr Ala Ser
 129 195 200 205
 131 Asp Val Trp Met Phe Ala Val Cys Met Trp Glu Ile Leu Ser Phe Gly
 132 210 215 220
 134 Lys Gln Pro Phe Phe Trp Leu Glu Asn Lys Asp Val Ile Gly Val Leu
 135 225 230 235 240
 137 Glu Lys Gly Asp Arg Leu Pro Lys Pro Asp Leu Cys Pro Pro Val Leu
 138 245 250 255

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140 Tyr Thr Leu Met Thr Arg Cys Trp Asp Tyr Asp Pro Ser Asp Arg Pro
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146 Lys Asp Ile Ala Met
147 290
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157 tatgaaggtg tctacacaaa tcacaaaggg gagaaaatca atgttagctgt caagacactgc 120
158 aagaaagact gcactctgga caacaaggag aagttcatga gcgaggcagt gatcatgaag 180
159 aacctcgacc acccgacat cgtaagctg atcggcatca ttgaagagga gcccacctgg 240
160 atcatcatgg aattgtatcc ctatggggag ctggccact acctggagcg gaacaagaac 300
161 tccctgaagg tgctcacccct cgtgctgtac tcactgcaga tatgcaaagc catggcctac 360
162 ctggagagca tcaactgcgt gcacaggagc attgctgtcc ggaacatcct ggtggcctcc 420
163 cctgagtgtg tgaagctggg ggacttttgtt cttcccggt acattgagga cgaggactat 480
164 tacaaggcct ctgtgactcg tctccccatc aaatggatgt ccccaagatc cattaactic 540
165 cgacgcttca cgacagccag tgacgtctgg atgttcgcgg tggcatgtg ggagatcctg 600
166 agctttggga agcagccctt cttctggctg gagaacaagg atgtcatcg ggtgctggag 660
167 aaaggagacc ggctgcccaa gcctgatctc tgtccaccgg tccttatac cctcatgacc 720
168 cgctgctggg actacgaccc cagtgaccgg ccccgcttca ccgagctggt gtgcagccctc 780
169 agtgcgttt atcagatgga gaaggacatt gccatg 816
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174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
179 pET15S nucleotide sequence
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182 tctagaaata attttggta actttaagaa ggagatatac catgggcagc agccatcatc 60
183 atcatcatca cagcagccgc ctgggccgc gcggcagcca tatgattgcc cgtgaagatg 120
184 tggcctgaa tcgtattctt ggggaaggct tttttggggg ggtctatgaa ggtgtctaca 180
185 caaatcacaa aggggagaaaa atcaatgtag ctgtcaagac ctgcaagaaa gactgcactc 240
186 tggacaacaa ggagaagttc atgagcgagg cagtgatcat gaagaacctc gaccacccgc 300
187 acatcgtaa gctgatccgc atcattgaag aggagccac ctggatcatc atggaattgt 360
188 atccctatgg ggagctggc cactacctgg agcggAACAA gaactccctg aaggtgctca 420
189 ccctcggtct gtactcaactg cagatatgca aagccatggc ctacctggag agcatcaact 480
190 gcgtgcacag ggacattgtct gtcggaaaca tcctggggc ctccctgtag tggatgtca 540
191 tgggggactt tggctttcc cgttacattg aggacgagga ctattacaaa gcctctgtga 600
192 ctcgtctccc catcaaattgg atgtccccag agtccattaa ctcccgacgc ttcacgacag 660
193 ccagtgcgt ctggatgttc gccgtgtgca tggatgtttt cctgagctt gggaaagcgc 720
194 ccttcttctg gctggagaac aaggatgtca tcgggggtgt ggagaaagga gaccggctgc 780
195 ccaaggcctga tctctgtcca ccggccctt ataccctcat gaccggctgc tgggactacg 840
196 acccccagtga ccggcccccgc ttacccggc tggatgtcag cctcagtgac gtttatcaga 900
197 tggagaagga cattttccatg taqgtcqact aqagctcqca qtctcqacca tcatcatcat 960

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198 catcattaat aaaaggcgaa attccagcac actggcgccc gttacttagtg gatccggctg 1020
199 ctaacaaagc ccgaaaaggaa gctgagttgg 1050
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203 <211> LENGTH: 33
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial Sequence
207 <220> FEATURE:
208 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
210 <400> SEQUENCE: 5
211 tccacacgt atgattgccgttgaagatgt ggt 33
214 <210> SEQ ID NO: 6
215 <211> LENGTH: 34
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
220 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
222 <400> SEQUENCE: 6
223 ctctcgtcga cctacatggc aatgtccttc tcca 34
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229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <221> NAME/KEY: CDS
233 <222> LOCATION: (108)..(170)
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
237 pET15S multi-cloning site nucleotide sequence
239 <400> SEQUENCE: 7
240 agatctcgat cccgcgaaat taatacgact cactataggg gaattgtgag cggtataacaa 60
242 ttccccctcta gaaataattt tgttaacctt taagaaggag atatacc atg ggc agc 116
243 Met Gly Ser
244 1
246 agc cat cat cat cat cac agc agc ggc ctg gtg ccg cgc ggc agc 164
247 Ser His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser
248 5 10 15
250 cat atg ggatccggaa ttcaaaggccc tacgtcgact agaggctgca gtctcgacca 220
251 His Met
252 20
254 tcatcatcat catcattaat aaaaggcgaa attccagcac actggcgccc gttacttagtg 280
256 gatccggctg ctaacaaagc ccgaaaaggaa gctgagttgg ctgtcgccac cgctgagcaa 340
258 taactagcat aacccttgg ggcctctaaa cgggtcttga ggggttttt g 391
261 <210> SEQ ID NO: 8
262 <211> LENGTH: 21
263 <212> TYPE: PRT
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
268 pET15S multi-cloning site peptide sequence

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 274 Arg Gly Ser His Met
 275 20
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 282 <211> LENGTH: 310
 283 <212> TYPE: PRT
 284 <213> ORGANISM: Unknown Organism
 286 <220> FEATURE:
 287 <223> OTHER INFORMATION: Description of Unknown Organism: FAK tyrosine kinase
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 290 <400> SEQUENCE: 9
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 292 1 5 10 15
 294 Gln Phe Gly Asp Val His Gln Gly Ile Tyr Met Ser Pro Glu Asn Pro
 295 20 25 30
 297 Ala Leu Ala Val Ala Ile Lys Thr Cys Lys Asn Cys Thr Ser Asp Ser
 298 35 40 45
 300 Val Arg Glu Lys Phe Leu Gln Glu Ala Cys His Tyr Thr Ser Leu His
 301 50 55 60
 303 Trp Asn Trp Cys Arg Tyr Ile Ser Asp Pro Asn Val Asp Ala Cys Pro
 304 65 70 75 80
 306 Asp Pro Arg Asn Ala Glu Leu Thr Met Arg Gln Phe Asp His Pro His
 307 85 90 95
 309 Ile Val Lys Leu Ile Gly Val Ile Thr Glu Asn Pro Val Trp Ile Ile
 310 100 105 110
 312 Met Glu Leu Cys Thr Leu Gly Glu Leu Arg Ser Phe Leu Gln Val Arg
 313 115 120 125
 315 Lys Tyr Ser Leu Asp Leu Ala Ser Leu Ile Leu Tyr Ala Tyr Gln Leu
 316 130 135 140
 318 Ser Thr Ala Leu Ala Tyr Leu Glu Ser Lys Arg Phe Val His Arg Asp
 319 145 150 155 160
 321 Ile Ala Ala Arg Asn Val Leu Val Ser Ser Asn Asp Cys Val Lys Leu
 322 165 170 175
 324 Gly Asp Phe Gly Leu Ser Arg Tyr Met Glu Asp Ser Thr Tyr Tyr Lys
 325 180 185 190
 327 Ala Ser Lys Gly Lys Leu Pro Ile Lys Trp Met Ala Pro Glu Ser Ile
 328 195 200 205
 330 Asn Phe Arg Arg Phe Thr Ser Ala Ser Asp Val Trp Met Phe Gly Val
 331 210 215 220
 333 Cys Met Trp Glu Ile Leu Met His Gly Val Lys Pro Phe Gln Gly Val
 334 225 230 235 240
 336 Lys Asn Asn Asp Val Ile Gly Arg Ile Glu Asn Gly Glu Arg Leu Pro
 337 245 250 255
 339 Met Pro Pro Asn Cys Pro Pro Thr Leu Tyr Ser Leu Met Thr Lys Cys
 340 260 265 270
 342 Trp Ala Tyr Asp Pro Ser Arg Arg Pro Arg Phe Thr Glu Leu Lys Ala
 343 275 280 285

VERIFICATION SUMMARY

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